

## SEQUENCE LISTING

<110> REGENTS OF THE UNIVERSITY OF CALIFORNIA  
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 TING, Alice  
 ZHANG, Jin

<120> EMISSION RATIONOMETRIC INDICATORS OF PHOSPHORYLATION

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<160> 42

<170> PatentIn version 3.0

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<213> Aequorea victoria

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gaa tta gat ggt gat gtt aat ggg cac aaa ttt tct gtc agt gga gag	96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
20 25 30	
ggt gaa ggt gat gca aca tac gga aaa ctt acc ctt aaa ttt att tgc	144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
35 40 45	
act act gga aaa cta cct gtt cca tgg cca aca ctt gtc act act ttc	192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
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tct tat ggt gtt caa tgc ttt tca aga tac cca gat cat atg aaa cag	240
Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln	
65 70 75 80	
cat gac ttt ttc aag agt gcc atg ccc gaa ggt tat gta cag gaa aga	288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
85 90 95	
act ata ttt ttc aaa gat gac ggg aac tac aag aca cgt gct gaa gtc	336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
100 105 110	
aag ttt gaa ggt gat acc ctt gtt aat aga atc gag tta aaa ggt att	384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
115 120 125	
gat ttt aaa gaa gat gga aac att ctt gga cac aaa ttg gaa tac aac	432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
130 135 140	

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Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile

115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn  
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly  
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val  
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro  
180 185 190

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser  
195 200 205

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val  
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gtc	gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	ttc	agc	gtg	tcc	ggc	96
Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	
			20					25					30			
gag	ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc	144
Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	
			35				40					45				
tgc	acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	192
Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	
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ctg	acc	tac	ggc	gtg	cag	tgc	ttc	agc	cgc	tac	ccc	gac	cac	atg	aag	240
Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	
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 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
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cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336  
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu  
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gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384  
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly  
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atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432  
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr  
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 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn  
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 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser  
                     165                    170                    175

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                     180                    185                    190

ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc gcc ctg 624  
 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu  
                     195                    200                    205

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 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe  
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gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag taa 720  
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Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
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Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr

"T04330" 1629360

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 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
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 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu  
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 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly  
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 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr  
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 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn  
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 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser  
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 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly  
                     180                      185                      190  
 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu  
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 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe  
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 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
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 gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144  
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
 35 40 45  
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 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
 50 55 60  
 ttc ggc tac ggc gtg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240  
 Phe Gly Tyr Gly Val Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys  
 65 70 75 80  
 cag cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288  
 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
 85 90 95  
 cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336  
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu  
 100 105 110  
 gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384  
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly  
 115 120 125  
 atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432  
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr  
 130 135 140  
 aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac 480  
 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn  
 145 150 155 160  
 ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc 528  
 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser  
 165 170 175  
 gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac ggc 576  
 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly  
 180 185 190  
 ccc gtg ctg ctg ccc gac aac cac tac ctg agc tac cag tcc gcc ctg 624

104250-1629960



Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu  
195 200 205

agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag ttc 672  
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe  
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35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
50 55 60

Phe Gly Tyr Gly Val Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys  
65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu  
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly  
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr  
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn  
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser  
165 170 175

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Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly  
180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu  
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Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe  
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Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
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Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
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Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
35 40 45  
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192  
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
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ttc ggc tac ggc ctg aag tgc ttc gcc cgc tac ccc gac cac atg aag 240  
Phe Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys  
65 70 75 80  
cag cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288  
Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
85 90 95  
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336  
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu  
100 105 110  
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384  
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly  
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Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr  
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Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn  
145 150 155 160

ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc 528  
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser  
165 170 175

gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac ggc 576  
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly  
180 185 190

ccc gtg ctg ctg ccc gac aac cac tac ctg agc tac cag tcc gcc ctg 624  
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu  
195 200 205

agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag ttc 672  
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe  
210 215 220

gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag taa 720  
Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
225 230 235

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<213> Aequorea victoria

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Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
50 55 60

Phe Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys  
65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu  
100 105 110

T04250" T6259550



Lys Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Phe  
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cag tat gga agc aag gta tat gtc aag cac cct gcc gac ata cca gac 296  
 Gln Tyr Gly Ser Lys Val Tyr Val Lys His Pro Ala Asp Ile Pro Asp  
 70 75 80

tat aaa aag ctg tca ttt cct gaa gga ttt aaa tgg gaa agg gtc atg 344  
 Tyr Lys Lys Leu Ser Phe Pro Glu Gly Phe Lys Trp Glu Arg Val Met  
 85 90 95

aac ttt gaa gac ggt ggc gtc gtt act gta acc cag gat tcc agt ttg 392  
 Asn Phe Glu Asp Gly Gly Val Val Thr Val Thr Gln Asp Ser Ser Leu  
 100 105 110

cag gat ggc tgt ttc atc tac aag gtc aag ttc att ggc gtg aac ttt 440  
 Gln Asp Gly Cys Phe Ile Tyr Lys Val Lys Phe Ile Gly Val Asn Phe  
 115 120 125

cct tcc gat gga cct gtt atg caa aag aag aca atg ggc tgg gaa gcc 488  
 Pro Ser Asp Gly Pro Val Met Gln Lys Lys Thr Met Gly Trp Glu Ala  
 130 135 140 145

agc act gag cgt ttg tat cct cgt gat ggc gtg ttg aaa gga gag att 536  
 Ser Thr Glu Arg Leu Tyr Pro Arg Asp Gly Val Leu Lys Gly Glu Ile  
 150 155 160

cat aag gct ctg aag ctg aaa gac ggt ggt cat tac cta gtt gaa ttc 584  
 His Lys Ala Leu Lys Leu Lys Asp Gly Gly His Tyr Leu Val Glu Phe  
 165 170 175

aaa agt att tac atg gca aag aag cct gtg cag cta cca ggg tac tac 632  
 Lys Ser Ile Tyr Met Ala Lys Lys Pro Val Gln Leu Pro Gly Tyr Tyr  
 180 185 190

tat gtt gac tcc aaa ctg gat ata aca agc cac aac gaa gac tat aca 680  
 Tyr Val Asp Ser Lys Leu Asp Ile Thr Ser His Asn Glu Asp Tyr Thr  
 195 200 205

atc gtt gag cag tat gaa aga acc gag gga cgc cac cat ctg ttc ctt 728  
 Ile Val Glu Gln Tyr Glu Arg Thr Glu Gly Arg His His Leu Phe Leu  
 210 215 220 225

taa ggctgaactt ggctcagacg tgggtgagcg gtaatgacca caaaaggcag 781

cgaagaaaaa ccatgatcgt tttttttagg ttggcagcct gaaatcgtag gaaatacatc 841

agaaatgtta caaacagg 859

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10450 "T633360"

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Gly Glu Gly Arg Pro Tyr Glu Gly His Asn Thr Val Lys Leu Lys Val  
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Thr Lys Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln  
50 55 60

Phe Gln Tyr Gly Ser Lys Val Tyr Val Lys His Pro Ala Asp Ile Pro  
65 70 75 80

Asp Tyr Lys Lys Leu Ser Phe Pro Glu Gly Phe Lys Trp Glu Arg Val  
85 90 95

Met Asn Phe Glu Asp Gly Gly Val Val Thr Val Thr Gln Asp Ser Ser  
100 105 110

Leu Gln Asp Gly Cys Phe Ile Tyr Lys Val Lys Phe Ile Gly Val Asn  
115 120 125

Phe Pro Ser Asp Gly Pro Val Met Gln Lys Lys Thr Met Gly Trp Glu  
130 135 140

Ala Ser Thr Glu Arg Leu Tyr Pro Arg Asp Gly Val Leu Lys Gly Glu  
145 150 155 160

Ile His Lys Ala Leu Lys Leu Lys Asp Gly Gly His Tyr Leu Val Glu  
165 170 175

Phe Lys Ser Ile Tyr Met Ala Lys Lys Pro Val Gln Leu Pro Gly Tyr  
180 185 190

Tyr Tyr Val Asp Ser Lys Leu Asp Ile Thr Ser His Asn Glu Asp Tyr  
195 200 205

Thr Ile Val Glu Gln Tyr Glu Arg Thr Glu Gly Arg His His Leu Phe  
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Leu  
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Lys Gly

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Leu Arg Arg Ala Ser Leu Pro  
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T00250 "T5359350

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 <223> Reverse primer for PCR

<400> 27  
 cgaggagctc gctgccgccc gtgccgccc ggctggcgcg acggaggctg ccgccggtgc 60  
 cgctgcaga gtctgatgtc caaagtgtta gg 92

<210> 28  
 <211> 33  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Primer for PCR

<400> 28  
 cgtcgcgcca gcctgccagg caccggcggc agc 33

<210> 29  
 <211> 33  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Primer for PCR

<400> 29  
 gctgccgccc gtggctggca ggctggcgcg acg 33

<210> 30  
 <211> 32  
 <212> DNA

1. 2. 3. 4. 5. 6. 7. 8. 9. 10. 11. 12. 13. 14. 15. 16. 17. 18. 19. 20. 21. 22. 23. 24. 25. 26. 27. 28. 29. 30. 31. 32. 33. 34. 35. 36. 37. 38. 39. 40. 41. 42. 43. 44. 45. 46. 47. 48. 49. 50. 51. 52. 53. 54. 55. 56. 57. 58. 59. 60. 61. 62. 63. 64. 65. 66. 67. 68. 69. 70. 71. 72. 73. 74. 75. 76. 77. 78. 79. 80. 81. 82. 83. 84. 85. 86. 87. 88. 89. 90. 91. 92. 93. 94. 95. 96. 97. 98. 99. 100.

<213> Artificial sequence

<220>

<223> Primer for PCR

<400> 30

gcctccgtcg cgccgcactg ccaggcaccg gc

32

<210> 31

<211> 32

<212> DNA

<213> Artificial sequence

<220>

<223> Primer for PCR

<400> 31

gccggtgcct ggcagtgcgg cgcgacggag gc

32

<210> 32

<211> 7

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic peptide

<400> 32

Leu Arg Arg Ala Ser Leu Gly  
1 5

<210> 33

<211> 9

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic peptide

<400> 33

Ala Gln Arg Ser Thr Ser Thr Pro Asn  
1 5

<210> 34

<211> 6

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic peptide

<220>

<221> VARIANT

<222> (1)..(6)

<223> Xaa is any Animo Acid

T04290 T6253350

<400> 34

Arg Ser Xaa Ser Xaa Pro  
1 5

<210> 35

<211> 4

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic peptide

<220>

<221> VARIANT

<222> (3)..(3)

<223> Xaa is any Amino Acid

<400> 35

Arg Arg Xaa Ser  
1

<210> 36

<211> 4

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic peptide

<220>

<221> VARIANT

<222> (2)..(3)

<223> Xaa is any Amino Acid

<220>

<221> VARIANT

<222> (4)..(4)

<223> Xaa is Serine or Threonine

<400> 36

Arg Xaa Xaa Xaa  
1

<210> 37

<211> 4

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic peptide

<220>

<221> VARIANT

<222> (1)..(1)

<223> Xaa is Lysine or Arginine

T0450 T6259360

<220>  
 <221> VARIANT  
 <222> (2)..(3)  
 <223> Xaa is any Amino Acid

<220>  
 <221> VARIANT  
 <222> (4)..(4)  
 <223> Xaa is Serine or Threonine

<400> 37

Xaa Xaa Xaa Xaa  
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<210> 38  
 <211> 39  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Forward primer for PCR

<400> 38  
 gccgcccgcgca tgcattgggtt ccacgggaag ctgagccgg

39

<210> 39  
 <211> 99  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Reverse primer for PCR

<400> 39  
 taccatgagc tctgattgcy gagccatggt catgtactca gcttcctctt caggcttccc  
 agatccagag tgagacccca cgggttgctc taggcacag

60

99

<210> 40  
 <211> 35  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Forward primer for PCR

<400> 40  
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35

<210> 41  
 <211> 93  
 <212> DNA  
 <213> Artificial sequence

104230 "T629360

<220>

<223> Reverse primer for PCR

<400> 41

caccatgagc tcaaattcac cgtagatctc agaaccctca ccagaaccg gcttcccaga 60

tccagatgta gaccacaga cgtagtcag gcg 93

<210> 42

<211> 7

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic peptide

<220>

<221> VARIANT

<222> (2)..(2)

<223> Xaa is Arginine or Lysine

<220>

<221> VARIANT

<222> (3)..(3)

<223> Xaa is Phenylalanine, Arginine, Serine or Asparagine

<220>

<221> VARIANT

<222> (4)..(4)

<223> Xaa is Arginine, Histidine, Lysine

<220>

<221> VARIANT

<222> (5)..(5)

<223> Phosphorylated peptide

<220>

<221> VARIANT

<222> (6)..(6)

<223> Xaa is Tryptophan, Tyrosine, Phenylalanine, Leucine

<400> 42

Arg Xaa Xaa Xaa Ser Xaa Pro

1

5

"1639350" 034434